

## Association of Prostate Cancer With Rapid *N*-acetyltransferase 1 (NAT1\*10) in Combination With Slow *N*-acetyltransferase 2 Acetylator Genotypes in a Pilot Case-Control Study

David W. Hein,<sup>1\*</sup> Matthew A. Leff,<sup>1</sup> Naoko Ishibe,<sup>2</sup> Rashmi Sinha,<sup>3</sup> Harold A. Frazier,<sup>4</sup> Mark A. Doll,<sup>1</sup> Gong H. Xiao,<sup>1</sup> Martin C. Weinrich,<sup>5</sup> and Neil E. Caporaso<sup>2</sup>

<sup>1</sup> Department of Pharmacology and Toxicology, University of Louisville School of Medicine, Louisville, Kentucky

<sup>2</sup> Genetic Epidemiology Branch, National Cancer Institute, Bethesda, Maryland

<sup>3</sup> Nutritional Epidemiology Branch, National Cancer Institute, Bethesda, Maryland

<sup>4</sup> National Naval Medical Center, Bethesda, Maryland

<sup>5</sup> Department of Medicine, University of Louisville School of Medicine, Louisville, Kentucky

*N*-acetyltransferase-1 (NAT1) and *N*-acetyltransferase-2 (NAT2) are important in the metabolism of aromatic and heterocyclic amine carcinogens that induce prostate tumors in the rat. We investigated the association of genetic polymorphisms in NAT1 and NAT2, alone and in combination, with human prostate cancer. Incident prostate cancer cases and controls in a hospital-based case-control study were frequency-matched for age, race, and referral pattern. The frequency of slow acetylator NAT1 genotypes (NAT1\*14, \*15, \*17) was 5.8% in controls but absent in cases. In contrast, in comparison with all other NAT1 genotypes the putative rapid acetylator NAT1 genotype (NAT1\*10) was significantly higher in prostate cancer cases than

controls (OR, 2.17; 95% CI, 1.08–4.33;  $P = 0.03$ ). Combinations of NAT1\*10 with NAT2 slow acetylator genotypes (OR, 5.08; 95% CI, 1.56–16.5;  $P = 0.008$ ) or with NAT2 very slow (homozygous NAT2\*5) acetylator genotypes (OR, 7.50; 95% CI, 1.55–15.4;  $P = 0.016$ ) further increased prostate cancer risk. The results of this small pilot study suggest increased susceptibility to prostate cancer for subjects with combinations of NAT1\*10 and slow (particularly very slow) NAT2 acetylator genotypes. This finding should be investigated further in larger cohorts and in other ethnic populations. Environ. Mol. Mutagen. 40:161–167, 2002. © 2002 Wiley-Liss, Inc.

**Key words:** prostate cancer; *N*-acetyltransferase 1; *N*-acetyltransferase 2; acetylator genotype

### INTRODUCTION

Both environmental and genetic factors are considered important in the etiology of human prostate cancer [Mettlin, 1997]. Some studies suggest a role for well-done meat [Norrish et al., 1999] and cigarette smoking [Hsing et al., 1991; Sharpe and Siemizycki, 2001] in prostate cancer etiology, but the findings have been equivocal. Aromatic [Katayama et al., 1982; Ito et al., 1988; Shirai et al., 1990] and heterocyclic [Shirai et al., 1997, 1999] amine carcinogens induce prostate tumors in the rat. The *N*-hydroxy metabolites of these carcinogens exhibit increased carcinogenicity [Shirai et al., 1992; Archer et al., 2000]. Humans are exposed to these carcinogens in cigarette smoke [Manabe et al., 1991; Peluso et al., 1991] and well-cooked foods [Layton et al., 1995; Bogen and Keating, 2001]

Hepatic *N*-acetylation of aromatic amines competes with hepatic *N*-hydroxylation, whereas *O*-acetylation of the *N*-hydroxy metabolites in target tissues yields unstable ace-

toxy intermediates, resulting in electrophiles that initiate tumors [Hein et al., 2000a]. These acetylation reactions are catalyzed by *N*-acetyltransferase 1 (NAT1) and 2 (NAT2) and these enzymes exhibit genetic polymorphism in humans [Hein et al., 2000a].

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Current address for H.A. Frazier: Department of Urology, George Washington University, Washington, DC.

\*Correspondence to: David W. Hein, Department of Pharmacology and Toxicology, University of Louisville School of Medicine, Louisville, KY 40292. E-mail: d.hein@louisville.edu

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Polymorphisms in *NAT1* yield over 25 variant alleles compared to the reference *NAT1*\*4 allele [Hein et al., 2000a]. A common *NAT1* allelic variant (*NAT1*\*10) is associated with increased acetyltransferase catalytic activity (rapid acetylator phenotype) in vitro [Bell et al., 1995a] and in vivo [Hein et al., 2000b]. The *NAT1*\*10 acetylator phenotype is somewhat controversial because the increased catalytic activity has not been consistently reported in other studies [reviewed in Hein et al., 2000a]. Other less common *NAT1* allelic variants (*NAT1*\*14, \*15, \*17, and \*22) are associated with reduced *N*- and *O*-acetyltransferase catalytic activities [Butcher et al., 1998; Lin et al., 1998; Fretland et al., 2001a, 2002; Hein, 2002].

Single nucleotide polymorphisms (SNPs) have been identified in *NAT2*, yielding over 25 variant alleles compared to the reference *NAT2*\*4 allele [Hein et al., 2000a]. Several of the SNPs result in alleles encoding for *NAT2* proteins with reduced activity, but G<sup>191</sup>A (R<sup>64</sup>Q) and T<sup>341</sup>C (I<sup>114</sup>T) found in the *NAT2*\*5 and *NAT2*\*14 clusters result in the greatest reduction in *NAT2* activity [Fretland et al., 2001b; Hein, 2002]. Slow acetylator phenotype (homozygous slow *NAT2* alleles) is associated with higher susceptibility to urinary bladder cancer upon exposure to aromatic amine carcinogens [Cartwright et al., 1982; Risch et al., 1995; Marcus et al., 2000]. In some studies, the association with urinary bladder cancer is greatest in the slowest *NAT2* acetylator phenotypes [Cartwright et al., 1982] or those possessing *NAT2*\*5 genotypes [Brockmoller et al., 1996; Okkels et al., 1997; Filiadis et al., 1999].

If exposures to aromatic and/or heterocyclic arylamines are important in human prostate cancer etiology, individual risk should be modified by genetic polymorphism in enzymes that biotransform them. Since *N*-acetyltransferase 2 is expressed predominantly in liver, we hypothesized that individuals with the slow acetylator *NAT2* genotype (particularly the very slow *NAT2* acetylator genotype) would be at increased risk. The rationale for this hypothesis is that very slow *NAT2* acetylators should have reduced hepatic *N*-acetylation of aromatic amine prostate carcinogens (detoxification) and therefore higher levels of hepatic *N*-hydroxylation (activation). Since *NAT1* is expressed in prostate [Agundez et al., 1998; Lawson and Kolar, 2002], we further hypothesized that following transport of the *N*-hydroxylated metabolite(s) to the prostate, individuals with rapid *NAT1* acetylator genotype have greater activation (*O*-acetylation) and therefore higher risk of prostate cancer. Individuals with a combination of rapid *NAT1* and slow *NAT2* acetylator genotypes would be at greater risk for prostate cancer. We tested this hypothesis in a pilot hospital-based case-control study.

## MATERIALS AND METHODS

### Study Population

Fifty-seven men over the age of 50 with newly diagnosed, pathologically confirmed cancer of the prostate identified at the National Naval Medical

Center (Bethesda, MD) were enrolled into the Genetics, Environment, and Metabolism Study from August 1993 to April 1995. Controls (127) were recruited from referrals from clinic physicians and from self-referrals generated by a recruitment flyer. Individuals with a previous diagnosis of malignancies (with the exception of skin cancer in situ) or other major medical illnesses were excluded. Hospital controls meeting the inclusion criteria were frequency-matched to the prostate cancer cases on age ( $\pm 5$  years), race, and referral pattern. Approximately 70% of the eligible subjects (57 of 82 eligible prostate cancer cases and 127 of 184 eligible controls) participated in the study. The primary reason for nonparticipation was subject refusal.

### Data Collection

Information on potential risk factors, such as demographics, family history, smoking history, and other lifestyle variables were collected by trained interviewers and use of a self-administered questionnaire. Information on dietary intake and family history data was ascertained for each subject by self-administered questionnaires. Blood samples from the study participants were also collected at a second study visit. Upon collection, the samples were centrifuged and aliquoted into plasma, buffy coat, and red blood cell components. DNA was obtained from buffy coat by using a standard organic method for DNA extraction.

### Genotype Determinations

*NAT1* genotype was determined using a polymerase chain reaction (PCR) restriction fragment length polymorphism (RFLP) assay as previously described [O'Neil et al., 2000]. The assay is designed to distinguish over 20 human *NAT1* alleles (*NAT1*\*3, \*4, \*5, \*10, \*11, \*14A, \*14B, \*15, \*16, \*17, \*18A, \*18B, \*19, \*20, \*21, \*22, \*24, \*25, \*26A, \*26B, and \*28).

*NAT2* genotype was determined using a PCR-RFLP assay previously described [Deitz et al., 2000] that is designed to distinguish over 25 human *NAT2* alleles (*NAT2*\*4, \*5A,B,C,D,E,F, \*6A,B,C,D,E, \*7A,B, \*11, \*12A,B,C, \*13, \*14A,B,C,D,E,F,G, \*17, \*18).

All analyses were conducted with laboratory personnel blinded to case status. Positive and negative controls were used to ensure the activity of enzymes and reagents and to ensure that samples were not contaminated with foreign DNA. Any ambiguous result was repeated and/or confirmed by automated sequencing. Random samples were confirmed for genotype determination using a Taqman allele discrimination method for determination of *NAT1* [Doll and Hein, 2002] or *NAT2* [Doll and Hein, 2001] genotype.

### Statistical Analyses

Crude odds ratios (OR) and 95% confidence intervals (95% CI) were calculated by Fisher's Exact Test. Chi-square tests were used to test the statistical significance of trends involving more than two categories. All *P* values were based on two-sided hypothesis tests. The absence of cases with slow *NAT1* genotype required a substitution of 0.5 for 0 in order to generate the OR. Subjects were frequency-matched to assure similar numbers of subjects in major age strata. Residual small differences in the age distribution were corrected using an age and race term in the logistic regression model. Results were adjusted for race, age, body mass index (BMI), smoking history, and/or family history of prostate cancer. Since these adjustments did not change the results, the unadjusted findings are presented. Since the number of slow acetylator *NAT1* genotypes was very low, all nonrapid *NAT1* genotypes were combined to serve as the reference group. Similarly, because of the small number of homozygous rapid *NAT2* acetylators, homozygous rapid and heterozygous *NAT2* acetylators (possessing *NAT2*\*4, \*12 or \*13) were combined to serve as the reference group. Since there were only nine subjects who were current smokers, current and past smokers were collapsed into a single group.

**TABLE I. Descriptive Statistics of Study Population**

Variable	Controls (%)	Cases (%)	P value
Age (years)	68.9 ± 7.3	69.0 ± 7.1	0.91
Body Mass Index	21.8 ± 3.3	21.8 ± 2.9	0.99
Race (% Caucasian)	94.4%	90.6%	
Education (years) <sup>a</sup>			
1–8	1 (0.8%)	1 (1.9%)	
9–12	10 (8.0%)	7 (13.2%)	
College	42 (33.6%)	16 (30.2%)	
Graduate	72 (57.6%)	29 (54.7%)	0.65
Smoking History <sup>a</sup>			
Never	44 (35.2%)	17 (32.1%)	
Ever	74 (59.2%)	34 (64.8%)	
Current	7 (5.6%)	2 (3.8%)	0.78
Pack-years <sup>b</sup>	28.3 ± 25.1	23.9 ± 22.7	0.36

<sup>a</sup>Information on education and smoking history not available for two controls and four cases.

<sup>b</sup>Based on smokers only (74 controls and 34 cases).

**TABLE II. NAT1 Alleles and Prostate Cancer**

NAT1 allele	Controls (%)	Cases (%)
3	6 (2.5)	0 (0)
4	183 (75.6)	70 (74.5)
10	42 (17.4)	22 (23.4)
11	4 (1.7)	2 (2.1)
14	5 (2.1)	0 (0)
15	1 (0.4)	0 (0)
17	1 (0.4)	0 (0)
Total	242 (100)	94 (100)

## RESULTS

Descriptive information was obtained from 53/57 cases and 125/127 controls (Table I). Over 90% of the cohort was Caucasian with a mean age of about 69 years at the time of the study. Over 50% of both cases and controls had a smoking history. The cases and controls did not differ significantly with respect to age, BMI, race, education, or smoking history (Table I).

The frequencies of NAT1 alleles and genotypes in cases and controls are shown in Tables II and III. The NAT1\*4 allele and the NAT1\*4/\*4 genotype were most common in this Caucasian population, followed by NAT1\*10 allele and NAT1\*4/\*10 genotype. As shown in Table II, the NAT1\*14, \*15, \*17 alleles, associated with slow acetylator phenotype, were observed only among the controls. In contrast, the frequency of the NAT1\*10 allele was higher in cases (23.4%) than controls (17.4%). As shown in Table III and summarized in Table IV, the rapid NAT1 genotype (NAT1\*10) was overrepresented in prostate cancer (OR, 2.17; 95% CI, 1.08–4.33). This effect of NAT1\*10 genotype on prostate cancer risk was observed in ever smokers (OR, 2.59; 95% CI, 1.13–5.96) but not in never smokers (OR, 0.98; 95% CI, 0.26–3.71).

The frequency of NAT2 alleles in cases and controls is

**TABLE III. NAT1 Genotype and Prostate Cancer**

NAT1 genotype	Controls (%)	Cases (%)
3/4	4 (3.3)	0
3/10	1 (0.8)	0
3/11	1 (0.8)	0
4/4	73 (60.3)	23 (48.9)
4/10	26 (21.5)	22 (46.8)
4/11	1 (0.8)	2 (4.3)
4/14	5 (4.5)	0
4/17	1 (0.8)	0
10/10	7 (5.8)	0
10/15	1 (0.8)	0
11/11	1 (0.8)	0
Total	121 (100)	47 (100)

**TABLE IV. NAT1 Genotype and Prostate Cancer**

NAT1 genotype	Controls (%)	Cases (%)	Crude OR (95% CI)
Not rapid (not NAT1*10)	86 (71.1)	25 (53.2)	1.0 (ref.)
Rapid (NAT1*10)	35 (28.9)	22 (46.8)	2.17 (1.08–4.33) <i>P</i> = 0.03

**TABLE V. NAT2 Allelic Frequencies in Prostate Cancer**

NAT2 Allele	Controls (%)	Cases (%)
4	53 (23.0)	15 (16.0)
12A	2 (0.9)	1 (1.1)
13	3 (1.3)	0
Subtotal Rapid	58 (25.2)	16 (17.0)
6A	72 (31.3)	30 (31.9)
7B	3 (1.3)	1 (1.1)
Subtotal, *6, *7	75 (32.6)	31 (33.0)
5A	5 (2.2)	0
5B	90 (39.1)	44 (46.8)
5C	2 (0.9)	2 (2.1)
14B	0	1 (1.1)
Subtotal *5, *14	97 (42.2)	47 (50.0)

shown in Table V. The most frequent NAT2 alleles in both cases and controls were NAT2\*5B > NAT2 6A > NAT2\*4. The frequency of rapid NAT2 acetylator alleles was higher in controls (25.2%) than cases (17.0%), whereas the frequency of very slow acetylator NAT2 alleles (NAT2\*5 and NAT2\*14) was lower in controls (42.2%) than cases (50.0%). The frequency of NAT2 genotypes in cases and controls is shown in Table VI. The slow NAT2 acetylator genotype was not significantly associated with prostate cancer (OR, 1.78; 95% CI, 0.88–3.60). The association between individuals homozygous for NAT2\*5 alleles (possessing T<sup>341</sup>C) and prostate cancer (OR, 2.43; 95% CI, 0.96–6.12) approached significance (*P* = 0.08). The slow NAT2 acetylator genotype was not associated with prostate cancer when stratified for smoking (data not shown).

Based on the considerations indicated earlier, if we postulate that rapid NAT1 and slow NAT2 are risk factors and

**TABLE VI. NAT2 Genotypes in Prostate Cancer**

NAT2 genotype	Controls (%)	Cases (%)	Crude OR (95% CI)
4/4	3 (2.6)	0	
4/5B	23 (19.8)	7 (14.9)	
4/5C	0	1 (2.1)	
4/6A	22 (19.0)	7 (14.9)	
4/7B	2 (1.7)	0	
5B/13	2 (1.7)	0	
5B/12A	2 (1.7)	0	
6A/13	1 (0.9)	0	
12A/14B	0	1 (2.1)	
Total Rapid	55 (47.8)	16 (34.0)	1.0 (ref.)
5A/5B	2 (1.7)	0	
5A/6A	3 (2.6)	0	
5B/5B	14 (12.1)	12 (25.5)	
5B/5C	1 (0.9)	0	
5B/6A	31 (26.7)	12 (25.5)	
5B/7B	1 (0.9)	1 (2.1)	
5C/6A	1 (0.9)	1 (2.1)	
6A/6A	7 (6.0)	5 (10.6)	
Total Slow	60 (52.2)	31 (66.0)	1.78 (0.88–3.60) <i>P</i> = 0.12
Subtotal *5/*5	17 (14.8)	12 (25.5)	2.43 (0.96–6.12) <i>P</i> = 0.08

**TABLE VII. Combination NAT2/NAT1\*10 Genotypes in Prostate Cancer**

NAT2/NAT1 at risk genotypes <sup>a</sup>	Controls (%)	Cases (%)	Crude OR (95% CI) <sup>a</sup>
0	36 (31.3)	6 (13.3)	1.0 (Ref.)
1	66 (57.4)	28 (62.2)	2.55 (0.96–6.72) <i>P</i> = 0.058
2	13 (11.3)	11 (24.4)	5.08 (1.56–16.5) <i>P</i> = 0.008
2 <sup>b</sup>	4 (3.5)	5 (11.1)	7.50 (1.55–15.4) <i>P</i> = 0.016

<sup>a</sup>At risk genotypes defined as NAT2 slow and NAT1 rapid acetylator (NAT1\*10) genotypes.

<sup>b</sup>NAT2 slow acetylator genotypes restricted to homozygous NAT2\*5.

evaluate risk based on the total number of “at risk” alleles observed, prostate cancer risk was 5-fold higher (OR, 5.08; 95% CI, 1.56–16.5; *P* = 0.008) for rapid NAT1 in combination with the slow NAT2 acetylator genotypes and over 7-fold higher (OR, 7.50; 95% CI, 1.55–15.4; *P* = 0.016) for rapid NAT1 in combination with the very slow (NAT2\*5) acetylator genotype (Table VII).

## DISCUSSION

The rapid NAT1 genotype (NAT1\*10) was associated with prostate cancer in this small pilot case-control study (OR, 2.17; 95% CI, 1.08–4.33; *P* = 0.03). This result is similar to a previous report that found a significant association (OR, 2.4; 95% CI, 1.0–5.6) between NAT1\*10 and prostate cancer in a Japanese population [Fukutome et al., 1999]. In addition to prostate cancer [Fukutome et al., 1999], associations of the NAT1\*10 genotype with breast

[Millikan et al., 1998; Krajinovic et al., 2001], colorectal [Bell et al., 1995b; Chen et al., 1998; Ishibe et al., 2002], urinary bladder [Taylor et al., 1998; Katoh et al., 1999; Cascorbi et al., 2001], oral [Katoh et al., 1998], lung [Wikman et al., 2001], larynx [Varzim et al., 2002], and gastric [Boissy et al., 2000] cancers have been reported. However, other studies have not found an association between the NAT1\*10 genotype and colorectal [Katoh et al., 2000; Butler et al., 2001; Houston and Tomlinson, 2001], urinary bladder [Vaziri et al., 2001], head and neck [Olshan et al., 2001; Fronhoffs et al., 2001], hepatitis B-related hepatocarcinoma [Yu et al., 2000], and childhood acute lymphoblastic anemia [Krajinovic et al., 2000]. The NAT1\*10 phenotype and its association with cancer susceptibility remain poorly understood [Brockton et al., 2000; Hein et al., 2000a; Hein, 2002].

The slow NAT2 acetylator genotype was not significantly associated with prostate cancer in this study (OR, 1.75; 95% CI, 0.86–3.54). However, the association between individuals homozygous for NAT2\*5 alleles (possessing T<sup>341</sup>C) and prostate cancer (OR, 2.43; 95% CI, 0.96–6.12) approached significance (*P* = 0.08). Recent studies investigating the relationship of NAT2 acetylator genotype and prostate cancer also did not find a significant association between NAT2 acetylator genotype and prostate cancer [Agundez et al., 1998; Wadelius et al., 1999]. These studies did not test the effect of NAT2\*5 separately.

Consistent with our hypothesis, prostate cancer risk was 5-fold higher (OR, 5.08; 95% CI, 1.56–16.5; *P* = 0.008) for rapid NAT1 in combination with the slow NAT2 acetylator genotypes and over 7-fold higher (OR, 7.50; 95% CI, 1.55–15.4; *P* = 0.016) in combination with the very slow (NAT2\*5) acetylator genotypes. The fact that NAT1\*10 is in linkage disequilibrium with the rapid NAT2\*4 acetylator genotype [Smelt et al., 1998; Henning et al., 1999; Cascorbi et al., 2001] may tend to mask the association of NAT1\*10 genotype with prostate cancer. Thus, we would expect the effect of NAT1\*10 on prostate cancer risk to be greater when not linked to rapid (i.e., NAT2\*4) acetylator genotype. Our findings suggest that *N*-acetylation via hepatic NAT2 is important in the detoxification of prostate carcinogens, whereas *O*-acetylation catalyzed by NAT1 expressed in prostate epithelial cells is important for their activation. Recent studies have measured *N*-acetyltransferase mRNA [Wang et al., 1999; Cui et al., 2000] and catalytic activity [Agundez et al., 1998; Yeh et al., 2000, 2001; Lawson and Kolar, 2002] in human prostate. Two of the studies [Agundez et al., 1998; Lawson and Kolar, 2002] clearly showed that human prostate *N*-acetyltransferase activity was catalyzed by NAT1 and not NAT2. Human prostate epithelial cells have been shown to activate heterocyclic amines [Williams et al., 2000; Lawson and Kolar, 2002] and *N*-hydroxy heterocyclic amines [Wang et al., 1999; Williams et al., 2000] to DNA adducts, which is consistent with the activation role for NAT1 within the prostate.



Previous studies have shown that the combination of the rapid *NAT1* acetylator genotype (*NAT1\*10*) with the slow *NAT2* acetylator genotype yielded the highest level of DNA adducts in human urinary bladder [Badawi et al., 1995] and the highest frequency of urinary bladder cancers [Taylor et al., 1998]. A similar finding has been reported recently for lung cancer [Wikman et al., 2001]. This is the first report of this finding for human prostate cancer, but the analogy is the same (i.e., one would expect the highest DNA adduct levels and prostate cancer frequency for the combination of rapid *NAT1* and slow *NAT2* acetylator genotypes). Thus, our pilot study suggests that the *NAT1* and *NAT2* acetylation polymorphisms both modify prostate cancer risk slightly, but in combination the increased risk is additive. It is likely that polymorphisms in other carcinogen-metabolizing enzymes also increase risk. The results of this small pilot study are consistent with our hypothesis but need to be confirmed in larger sample sizes and in other ethnic groups.

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*Accepted by—*  
F.F. Kadlubar